SEQUENCE LISTING

- <110> Magainin Pharmaceuticals, Inc.
- <120> Asthma-Associated Factors as Targets for Treating Atopic Allergies, Including Asthma and Related Disorders
- <130> 36870-5073-WO
- <140> PCT/US99/04703
- <141> 1999-03-03
- <150> US 08/697,360
- <151> 1996-08-23
- <150> US 08/697,419
- <151> 1996-08-23
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2786

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- Ile His Thr Val Ala Leu Gly Pro Ala Ala Ala Lys Glu Leu Glu Gln
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	aga Arg	agt Ser	gca Ala 275	tgg Trp	gat Asp	gta Val	atc Ile	aca Thr 280	gac Asp	tct Ser	gct Ala	gac Asp	ttt Phe 285	cac His	cac His	agc Ser	983
	ttt Phe	ecc Pro 290	atg Met	aac Asn	G] À aaa	act Thr	gag Glu 295	ctt Leu	cca Pro	cct Pro	cct Pro	ccc Pro 300	aca Thr	ttc Phe	tcg Ser	ctt Leu	1031
					gac Asp												1079
					gct Ala 325												1127

	+++	tat	++~	3 t G		_ 4_ 4_				1							
	Phe	Tyr	Leu	atg Met 340	Gln	Ile	Val	gaa Glu	Ile 345	His	Thr	Phe	gtg Val	Gly 350	Ile	gcc Ala	1175
	agt Ser	ttc Phe	gac Asp 355	agc Ser	aaa Lys	gga Gly	gag Glu	atc Ile 360	aga Arg	gcc Ala	cag Gln	cta Leu	cac His 365	caa Gln	att Ile	aac Asn	1223
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				agt Ser													1463
				aat Asn													1511
				eca Pro													1559
				tcc Ser													1607
				aca Thr 500													1655
				gtg Val													1703

acg Thr	tgg Trp 530	cag Gln	gcc Ala	agt Ser	ggt Gly	cct Pro 535	cct Pro	gag Glu	att Ile	ata Ile	tta Leu 540	ttt Phe	gat Asp	cct Pro	gat Asp	1751
gga Gly 545	cga Arg	aaa Lys	tac Tyr	tac Tyr	aca Thr 550	aat Asn	aat Asn	ttt Phe	atc Ile	acc Thr 555	aat Asn	cta Leu	act Thr	ttt Phe	cgg Arg 560	1799
aca Thr	gct Ala	agt Ser	ctt Leu	tgg Trp 565	att Ile	cca Pro	gga Gly	aca Thr	gct Ala 570	aag Lys	cct Pro	GJ À dad	cac His	tgg Trp 575	act Thr	1847
tac Tyr	acc Thr	ctg Leu	aac Asn 580	aat Asn	acc Thr	cat His	cat His	tct Ser 585	ctg Leu	caa Gln	gcc Ala	ctg Leu	aaa Lys 590	gtg Val	aca Thr	1895
, gtg Val	acc Thr	tct Ser 595	cgt Arg	gcc Ala	tcc Ser	aac Asn	tca Ser 600	gct Ala	gtg Val	ccc Pro	cca Pro	gcc Ala 605	act Thr	gtg Val	gaa Glu	1943
	ttt Phe 610															1991
tat Tyr 625	gcc Ala	aat Asn	gtg Val	aaa Lys	cag Gln 630	gga Gly	ttt Phe	tat Tyr	ccc Pro	att Ile 635	ctt Leu	aat Asn	gcc Ala	act Thr	gtc Val 640	2039
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	gat Asp															2135
	agg Arg															2183
	cat His 690															2231
	ggg Gly															,2279

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gaa Glu	ata Ile	aga Arg	atg Met	agt Ser 805	aaa Lys	agt Ser	cta Leu	cag Gln	aat Asn 810	atc Ile	caa Gln	gat Asp	gac Asp	ttt Phe 815	aac Asn	2567
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Ile Gly Ile Ile Cys Leu Ile Ile Val Val Thr His His Thr Leu Ser
915 920 925

agg aaa aag aga gca gac aag aaa gag aat gga aca aaa tta tta 2948 Arg Lys Lys Arg Ala Asp Lys Lys Glu Asn Gly Thr Lys Leu Leu 930 935 940

taaataaata too aaagtga ottoottott agatataaga cocatggoot togactacaa 3008
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caatacagat aagattttta catggtagat caacaaatto tttttggggg tagattagaa 3128
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Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn 35 40 45

Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met 50 55 60

Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val 65 70 75 80

Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Thr Trp Lys Ala Asn 85 90 95

Asn Asn Ser Lys Ile Lys Gln Glu Ser Tyr Glu Lys Ala Asn Val Ile 100 105 110

Val Thr Asp Trp Tyr Arg Ala His Gly Asp Asp Pro Tyr Thr Leu Gln

Tyr Arg Gly Cys Gly Lys Glu Gly Lys Tyr Ile His Phe Thr Pro Asn Phe Leu Leu Asn Asp Asn Leu Thr Ala Gly Tyr Gly Ser Arg Gly Arg Val Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp Lys Pro Phe Tyr Ile Asn Gly Gln Asn Gln Ile Lys Val Thr Arg Cys Ser Ser Asp Ile Thr Gly Ile Phe Val Cys Glu Lys - Gly Pro Cys Pro Gln Glu Asn Cys Ile Ile Ser Lys Leu Phe Lys Glu Gly Cys Thr Phe Ile Tyr Asn Ser Thr Gln Ser Ala Thr Ala Ser Ile Met Phe Met Arg Ser Leu Ser Ser Val Val Glu Phe Cys Asn Ala Ser Thr His Asn Gln Glu Ala Pro Asn Leu Gln Asn Gln Met Cys Ser Leu Arg Ser Ala Trp Asp Val Ile Thr Asp Ser Ala Asp Phe His His Ser Phe Pro Met Asn Gly Thr Glu Leu Pro Pro Pro Pro Thr Phe Ser Leu Val Glu Ala Gly Asp Lys Val Val Cys Leu Val Leu Asp Ala Ser Ser Lys Met Ala Glu Ala Asp Arg Leu Leu Gln Leu Gln Gln Ala Ala Glu Phe Tyr Leu Met Gln Ile Val Glu Ile His Thr Phe Val Gly Ile Ala 

Ser Phe Asp Ser Lys Gly Glu Ile Arg Ala Gln Leu His Gln Ile Asn

Ser Asn Asp Asp Arg Lys Leu Leu Val Ser Tyr Leu Pro Thr Thr Val

375

Glu Val Val Glu Lys Leu Asn Gly Lys Ala Tyr Gly Ser Val Met Ile 405 410 415

Leu Val Thr Ser Gly Asp Asp Lys Leu Leu Gly Asn Cys Leu Pro Thr 420 425 430

Val Leu Ser Ser Gly Ser Thr Ile His Ser Ile Ala Leu Gly Ser Ser 435 440 445

Ala Ala Pro Asn Leu Glu Glu Leu Ser Arg Leu Thr Gly Gly Leu Lys 450 455 460

Phe Phe Val Pro Asp Ile Ser Asn Ser Asn Ser Met Ile Asp Ala Phe 465 470 475 480

Ser Arg Ile Ser Ser Gly Thr Gly Asp Ile Phe Gln Gln His Ile Gln 485 490 495

Leu Glu Ser Thr Gly Glu Asn Val Lys Pro His His Gln Leu Lys Asn 500 505 510

Thr Val Thr Val Asp Asn Thr Val Gly Asn Asp Thr Met Phe Leu Val 515 520 525

Thr Trp Gln Ala Ser Gly Pro Pro Glu Ile Ile Leu Phe Asp Pro Asp 530 535 540

Gly Arg Lys Tyr Tyr Thr Asn Asn Phe Ile Thr Asn Leu Thr Phe Arg 545 550 555 560

Thr Ala Ser Leu Trp Ile Pro Gly Thr Ala Lys Pro Gly His Trp Thr 565 570 575

Tyr Thr Leu Asn Asn Thr His His Ser Leu Gln Ala Leu Lys Val Thr 580 585 590

Val Thr Ser Arg Ala Ser Asn Ser Ala Val Pro Pro Ala Thr Val Glu 595 600 605

Ala Phe Val Glu Arg Asp Ser Leu His Phe Pro His Pro Val Met Ile 610 615 620

Tyr Ala Asn Val Lys Gln Gly Phe Tyr Pro Ile Leu Asn Ala Thr Val

- Thr Ala Thr Val Glu Pro Glu Thr Gly Asp Pro Val Thr Leu Arg Leu 645 650 655
- Leu Asp Asp Gly Ala Gly Ala Asp Val Ile Lys Asn Asp Gly Ile Tyr 660 665 670
- Ser Arg Tyr Phe Phe Ser Phe Ala Ala Asn Gly Arg Tyr Ser Leu Lys
  675 680 685
- Val His Val Asn His Ser Pro Ser Ile Ser Thr Pro Ala His Ser Ile 690 695 700
- Pro Gly Ser His Ala Met Tyr Val Pro Gly Tyr Thr Ala Asn Gly Asn 705 710 715 720
- _ Ile Gln Met Asn Ala Pro Arg Lys Ser Val Gly Arg Asn Glu Glu Glu 725 730 735
  - Arg Lys Trp Gly Phe Ser Arg Val Ser Ser Gly Gly Ser Phe Ser Val
    740 745 750
  - Leu Gly Val Pro Ala Gly Pro His Pro Asp Val Phe Pro Pro Cys Lys
    755 760 765
  - Ile Ile Asp Leu Glu Ala Val Lys Val Glu Glu Glu Leu Thr Leu Ser 770 780
  - Trp Thr Ala Pro Gly Glu Asp Phe Asp Gln Gly Gln Ala Thr Ser Tyr
    785 790 795 800
  - Glu Ile Arg Met Ser Lys Ser Leu Gln Asn Ile Gln Asp Asp Phe Asn 805 810 815
  - Asn Ala Ile Leu Val Asn Thr Ser Lys Arg Asn Pro Gln Gln Ala Gly 820 825 830
  - Ile Arg Glu Ile Phe Thr Phe Ser Pro Gln Ile Ser Thr Asn Gly Pro 835 840 845
  - Glu His Gln Pro Asn Gly Glu Thr His Glu Ser His Arg Ile Tyr Val 850 855 860
  - Ala Ile Arg Ala Met Asp Arg Asn Ser Leu Gln Ser Ala Val Ser Asn 865 870 875 880
  - Ile Ala Gln Ala Pro Leu Phe Ile Pro Pro Asn Ser Asp Pro Val Pro

885 890 895 Ala Arg Asp Tyr Leu Ile Leu Lys Gly Val Leu Thr Ala Met Gly Leu 900 905 Ile Gly Ile Ile Cys Leu Ile Ile Val Val Thr His His Thr Leu Ser 920 925 Arg Lys Lys Arg Ala Asp Lys Lys Glu Asn Gly Thr Lys Leu Leu 930 935 <210> 5 <211> 2745 <212> DNA <213> Homo sapiens ~ <220> <221> CDS <222> (1)..(2742) <400> 5 atg ggg cca ttt aag agt tct gtg ttc atc ttg att ctt cac ctt cta 48 Met Gly Pro Phe Lys Ser Ser Val Phe Ile Leu Ile Leu His Leu Leu 1 5 10 gaa ggg gcc ctg agt aat tca ctc att cag ctg aac aac aat ggc tat 96 Glu Gly Ala Leu Ser Asn Ser Leu Ile Gln Leu Asn Asn Gly Tyr 20 25 30 gaa ggc att gtc gtt gca atc gac ccc aat gtg cca gaa gat gaa aca Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr 35 40 ctc att caa caa ata aag gac atg gtg acc cag gca tct ctg tat ctg 192 Leu Ile Gln Gln Ile Lys Asp Met Val Thr Gln Ala Ser Leu Tyr Leu 55 ttt gaa gct aca gga aag cga ttt tat ttc aaa aat gtt gcc att ttg 240

att cct gaa aca tgg aag aca aag gct gac tat gtg aga cca aaa ctt 288

Ile Pro Glu Thr Trp Lys Thr Lys Ala Asp Tyr Val Arg Pro Lys Leu

85 90 95

75

80

Phe Glu Ala Thr Gly Lys Arg Phe Tyr Phe Lys Asn Val Ala Ile Leu

70

65

gag acc tac aaa aat gct gat gtt ctg gtt gct gag tct act cct cca 336 Glu Thr Tyr Lys Asn Ala Asp Val Leu Val Ala Glu Ser Thr Pro Pro

ggt Gly	aat Asn	gat Asp 115	gaa Glu	ccc Pro	tac Tyr	act Thr	gag Glu 120	cag Gln	atg Met	ggc	aac Asn	tgt Cys 125	gga Gly	gag Glu	aag Lys	384
ggt Gly	gaa Glu 130	agg Arg	atc Ile	cac	ctc Leu	act Thr 135	cct Pro	gat Asp	ttc Phe	att Ile	gca Ala 140	gga Gly	aaa Lys	aag Lys	tta Leu	432
gct Ala 145	gaa Glu	tat Tyr	gga Gly	cca Pro	caa Gln 150	ggt Gly.	agg Arg	gca Ala	ttt Phe	gtc Val 155	cat His	gag Glu	tgg Trp	gct Ala	cat His 160	480
cta Leu	cga Arg	tgg Trp	gga Gly	gta Val 165	ttt Phe	gac Asp	gag Glu	tac Tyr	aat Asn 170	aat Asn	gat Asp	gag Glu	aaa Lys	ttc Phe 175	tac Tyr	528
tta Leu	tcc Ser	aat Asn	gga Gly 180	aga Arg	ata Ile	caa Gln	gca Ala	gta Val 185	aga Arg	tgt Cys	tca Ser	gca Ala	ggt Gly 190	att Ile	act Thr	576
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caa Gln	cat His	gtt Val	gat Asp	tct Ser 245	ata Ile	gtt Val	gaa Glu	ttc Phe	tgt Cys 250	aca Tḥr	gaa Glu	caa Gln	aac Asn	cac His 255	aac Asn	768
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tgg Trp	gaa Glu	gtg Val 275	atc Ile	cgt Arg	gat Asp	tct Ser	gag Glu 280	gac Asp	ttt Phe	aag Lys	aaa Lys	acc Thr 285	act Thr	cct Pro	atg Met	864
aca Thr	aca Thr	cag Gln	cca Pro	cca Pro	aat Asn	ccc Pro	acc Thr	ttc Phe	tca Ser	ttg Leu	ctg Leu	cag Gln	att Ile	gga Gly	caa Gln	912

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			atg Met														1392
			ggc Gly														1440
			tct Ser														1488

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	gtt Val	caa Gln	cac His	aag Lys	caa Gln 725	gtg Val	tgt Cys	ttc Phe	agc Ser	aga Arg 730	aca Thr	tcc Ser	tcg Ser	Gly	ggc Gly 735	tca Ser	2208
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•	cct Pro	ggc Gly	caa Gln 755	atc Ile	acc Thr	gac Asp	ctg Leu	aag Lys 760	gcg Ala	gaa Glu	att Ile	His	ggg Gly 765	ggc	agt Ser	ctc Leu	2304
	att Ile	aat Asn 770	ctg Leu	act Thr	tgg Trp	aca Thr	gct Ala 775	cct Pro	ggg Gly	gat Asp	gat Asp	tat Tyr 780	Asp	cat His	gga Gly	aca Thr	2352
	gct Ala 785	cac His	aag Lys	tat Tyr	atc Ile	att Ile 790	cga Arg	ata Ile	agt Ser	aca Thr	agt Ser 795	att Ile	ctt Leu	gat Asp	ctc Leu	aga Arg 800	2400
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							gaa Glu										2496
							gat Asp										2544
							gaa Glu 855						-	_		-	2592
							ccg Pro										2640

cac att tta aaa att atg tgg aag tgg ata gga gaa ctg cag ctg tca 2736 His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser 900 905 910

ata gcc tag 2745 Ile Ala

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~ <213> Homo sapiens

<400> 6

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Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr
35 40 45

Leu Ile Gln Gln Ile Lys Asp Met Val Thr Gln Ala Ser Leu Tyr Leu 50 55 60

Phe Glu Ala Thr Gly Lys Arg Phe Tyr Phe Lys Asn Val Ala Ile Leu 65 70 75 80

Ile Pro Glu Thr Trp Lys Thr Lys Ala Asp Tyr Val Arg Pro Lys Leu 85 90 95

Glu Thr Tyr Lys Asn Ala Asp Val Leu Val Ala Glu Ser Thr Pro Pro . 100 105 110

Gly Asn Asp Glu Pro Tyr Thr Glu Gln Met Gly Asn Cys Gly Glu Lys
115 120 125

Gly Glu Arg Ile His Leu Thr Pro Asp Phe Ile Ala Gly Lys Lys Leu 130 135 140

Ala Glu Tyr Gly Pro Gln Gly Arg Ala Phe Val His Glu Trp Ala His

- Leu Arg Trp Gly Val Phe Asp Glu Tyr Asn Asn Asp Glu Lys Phe Tyr 165 170 175
- Leu Ser Asn Gly Arg Ile Gln Ala Val Arg Cys Ser Ala Gly Ile Thr 180 185 190
- Gly Thr Asn Val Val Lys Lys Cys Gln Gly Gly Ser Cys Tyr Thr Lys 195 200 205
- Arg Cys Thr Phe Asn Lys Xaa Thr Gly Leu Tyr Glu Lys Gly Cys Glu 210 215 220
- Phe Val Leu Gln Ser Arg Gln Thr Glu Lys Ala Ser Ile Met Phe Ala 225 230 235 240
- Gln His Val Asp Ser Ile Val Glu Phe Cys Thr Glu Gln Asn His Asn 245 250 255
  - Lys Glu Ala Pro Asn Lys Gln Asn Gln Lys Cys Asn Leu Arg Ser Thr 260 265 270
  - Trp Glu Val Ile Arg Asp Ser Glu Asp Phe Lys Lys Thr Thr Pro Met 275 280 285
  - Thr Thr Gln Pro Pro Asn Pro Thr Phe Ser Leu Leu Gln Ile Gly Gln 290 295 300
  - Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Ala Thr Gly 305 310 315 320
  - Asn Arg Leu Asn Arg Leu Asn Gln Ala Gly Gln Leu Phe Leu Leu Gln 325 330 335
  - Thr Val Glu Leu Gly Ser Trp Val Gly Met Val Thr Phe Asp Ser Ala 340 345 350
  - Ala His Val Gln Ser Glu Leu Ile Gln Ile Asn Ser Gly Ser Asp Arg 355 360 365
  - Asp Thr Leu Ala Lys Arg Leu Pro Ala Ala Ala Ser Gly Gly Thr Ser 370 375 380
  - Ile Cys Ser Gly Leu Arg Ser Ala Phe Thr Val Ile Arg Lys Lys Tyr 385 390 395 400
  - Pro Thr Asp Gly Ser Glu Ile Val Leu Leu Thr Asp Gly Glu Asp Asn

Thr Ile Ser Gly Cys Phe Asn Glu Val Lys Gln Ser Gly Ala Ile Ile 

His Thr Val Ala Leu Gly Pro Ser Ala Ala Gln Glu Leu Glu Glu Leu 

Ser Lys Met Thr Gly Gly Leu Gln Thr Tyr Ala Ser Asp Gln Val Gln 

Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Ser Ser Gly Asn Gly 

Ala Val Ser Gln Arg Ser Ile Gln Leu Glu Ser Lys Gly Leu Thr Leu 

. Gln Asn Ser Gln Trp Met Asn Gly Thr Val Ile Val Asp Ser Thr Val 

Gly Lys Asp Thr Leu Phe Leu Ile Thr Trp Thr Thr Gln Pro Pro Gln 

Ile Leu Leu Trp Asp Pro Ser Gly Gln Lys Gln Gly Gly Phe Val Val 5.3-5 

Asp Lys Asn Thr Lys Met Ala Tyr Leu Gln Ile Pro Gly Ile Ala Lys 

Val Gly Thr Trp Lys Tyr Ser Leu Gln Ala Ser Ser Gln Thr Leu Thr 

Leu Thr Val Thr Ser Arg Ala Ser Asn Ala Thr Leu Pro Pro Ile Thr 

Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser Pro Leu 

Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Pro Ile Leu Arg Ala 

Ser Val Thr Ala Leu Ile Glu Ser Val Asn Gly Lys Thr Val Thr Leu 

Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly 

Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser

Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Val 

Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn 

Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp 

Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser 

Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro 

Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu 

Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr 

Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg 790 💉 

Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro 

Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile 

Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp 

Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu 

Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr 

Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile 

His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser 

Ile Ala

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<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: sense primer
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 <400> 7
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                                                                    24
 <210> 8
, <211> 24
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 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: anti-sense
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 <400> 8.
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                                                                    24
 <210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: sense primer
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 <211> 22
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 <213> Artificial Sequence
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<220>

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<223> Description of Artificial Sequence: anti-sense
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 <400> 10
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 <211> 21
 <212> DNA
 <213> Artificial Sequence
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                                                                    21
 <210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence
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       for ICACC-1
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                                                                    21
 <210> 13
 <211> 22
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: peptide for
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 Cys Leu Val Leu Asp Lys Ser Gly Ser Met Leu Asn Asp Asp Arg Leu
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                                                           15
 Asn Arg Met Asn Gln Ala
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 <211> 20
 <212> PRT
 <213> Artificial Sequence
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 <400> 14
 Gln Ser Glu Leu Lys Gln Leu Asn Ser Gly Ala Asp Arg Asp Leu Leu
 Ile Lys His Cys
 <210> 15
 <211> 25
 <212> PRT
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: peptide for
       immunization to mICACC-1
<400> 15
 Lys Lys Lys Tyr Pro Thr Asp Gly Ser Glu Ile Val Leu Leu Thr Asp
                   5
                                      10
 Gly Glu Asp Asn Thr Ile Ser Ser Cys
              20
                                   25
 <210> 16
 <211> 24
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: peptide for
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Gln Asn Gly Phe Ile Leu Asp Cys
20

<210> 17

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide for immunization to mICACC-1

<400> 17

Cys Pro Pro Ile Thr Val Thr Pro Val Val Asn Lys Asn Thr Gly Lys

1 10 15

Phe Pro Ser Pro Val Thr 20

<210> 18

<211> 903

<212> PRT

<213> Bos taurus

<400> 18

Met Val Pro Arg Leu Thr Val Ile Leu Phe Leu Thr Leu His Leu Leu 1 5 10 15

Pro Gly Met Lys Ser Ser Met Val Asn Leu Ile Asn Asn Gly Tyr Asp 20 25 30

Gly Ile Val Ile Ala Ile Asn Pro Ser Val Pro Glu Asp Glu Lys Leu 35 40 45

Ile Gln Asn Ile Lys Glu Met Val Thr Glu Ala Ser Thr Tyr Leu Phe 50 55 60

His Ala Thr Lys Arg Arg Val Tyr Phe Arg Asn Val Ser Ile Leu Ile 65 70 75 80

Pro Met Thr Trp Lys Ser Lys Ser Glu Tyr Leu Met Pro Lys Gln Glu 85 90 95

Ser Tyr Asp Gln Ala Glu Val Ile Val Ala Asn Pro Tyr Leu Lys His
100 105 110

- Gly Asp Asp Pro Tyr Thr Leu Gln Tyr Gly Arg Cys Gly Glu Lys Gly 115 120 125
- Gln Tyr Ile His Phe Thr Pro Asn Phe Leu Leu Thr Asn Asn Leu Pro 130 135 140
- Arg Trp Gly Ile Phe Asp Glu Tyr Asn Gly Asp Gln Pro Phe Tyr Ile 165 170 175
- Ser Arg Arg Asn Thr Ile Glu Ala Thr Arg Cys Ser Thr His Ile Thr 180 185 190
- Gly Thr Asn Val Ile Val Lys Cys Gln Gly Gly Ser Cys Ile Thr Arg 195 200 205
- Pro Cys Arg Arg Asp Ser Gln Thr Gly Leu Tyr Glu Ala Lys Cys Thr 210 215 220
- Phe Ile Pro Glu Lys Ser Gln Thr Ala Arg Glu Ser Ile Met Phe Met 225 230 235 240
- Gln Ser Leu His Ser Val Thr Glu Phe Cys Thr Glu Lys Thr His Asn 245 250 255
- Val Glu Ala Pro Asn Leu Gln Asn Lys Met Cys Asn Gly Lys Ser Thr 260 265 270
- Trp Asp Val Ile Met Asn Ser Thr Asp Phe Gln Asn Thr Ser Pro Met 275 280 285
- Thr Glu Met Asn Pro Pro Thr Gln Pro Thr Phe Ser Leu Leu Lys Ser 290 295 300
- Lys Gln Arg Val Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Ser 305 310 315 320
- Ser Glu Asp Arg Leu Phe Arg Met Asn Gln Ala Ala Glu Leu Phe Leu 325 330 335
- Ile Gln Ile Ile Glu Lys Gly Ser Leu Val Gly Met Val Thr Phe Asp 340 345 350
- Ser Val Ala Glu Ile Arg Asn Asn Leu Thr Lys Ile Thr Asp Asp Asn 355 360 365

- Val Tyr Glu Asn Ile Thr Ala Asn Leu Pro Gln Glu Ala Asn Gly Gly 370 380
- Thr Ser Ile Cys Arg Gly Leu Lys Ala Gly Phe Gln Ala Ile Ile Gln 385 390 395 400
- Ser Gln Gln Ser Thr Ser Gly Ser Glu Ile Ile Leu Leu Thr Asp Gly 405 410 415
- Glu Asp Asn Glu Ile His Ser Cys Ile Glu Glu Val Lys Gln Ser Gly 420 425 430
- Val Ile Ile His Thr Ile Ala Leu Gly Pro Ser Ala Ala Lys Glu Leu 435 440 445
- Glu Thr Leu Ser Asp Met Thr Gly Gly His Arg Phe Tyr Ala Asn Lys
  450
  460
- Asp Ile Asn Gly Leu Thr Asn Ala Phe Ser Arg Ile Ser Ser Arg Ser 465 470 475 480
- Gly Ser Ile Thr Gln Gln Thr Ile Gln Leu Glu Ser Lys Ala Leu Ala 485 490 495
- Ile Thr Glu Lys Lys Trp Val Asn Gly Thr Val Pro Val Asp Ser Thr 500 505 510
- Ile Gly Asn Asp Thr Phe Phe Val Val Thr Trp Thr Ile Lys Lys Pro 515 520 525
- Glu Ile Leu Leu Gln Asp Pro Lys Gly Lys Lys Tyr Lys Thr Ser Asp 530 535 540
- Phe Lys Glu Asp Lys Leu Asn Ile His Ser Ala Arg Leu Arg Ile Pro 545 550 555 560
- Gly Ile Ala Glu Thr Gly Thr Trp Thr Tyr Ser Leu Leu Asn Asn His 565 570 575
- Ala Ser Pro Gln Ile Leu Thr Val Thr Val Thr Thr Arg Ala Arg Ser 580 585 590
- Pro Thr Thr Pro Pro Val Thr Ala Thr Ala His Met Ser Gln Asn Thr 595 600 605
- Ala His Tyr Pro Ser Pro Val Ile Val Tyr Ala Gln Val Ser Gln Gly 610 620

Phe Leu Pro Val Leu Gly Ile Asn Val Thr Ala Ile Ile Glu Thr Glu Asp Gly His Gln Val Thr Leu Glu Leu Trp Asp Asn Gly Ala Gly Ala Asp Thr Val Lys Asn Asp Gly Ile Tyr Ser Arg Tyr Phe Thr Asp Tyr Arg Gly Asn Gly Arg Tyr Ser Leu Lys Val His Ala Glu Ala Arg Asn Asn Thr Ala Arg Leu Ser Leu Arg Gln Pro Gln Asn Lys Ala Leu Tyr Ile Pro Gly Tyr Ile Glu Asn Gly Lys Ile Ile Leu Asn Pro Pro Arg ~ 705 Pro Glu Val Lys Asp Asp Leu Ala Lys Ala Glu Ile Glu Asp Phe Ser Arg Leu Thr Ser Gly Gly Ser Phe Thr Val Ser Gly Ala Pro Pro Gly Asn His Pro Ser Val Leu Pro Pro Asn Lys Ile Ile Asp Leu Glu Ala Lys Phe Lys Glu Asp His Ile Gln Leu Ser Trp Thr Ala Pro Ala Asn Val Leu Asp Lys Gly Lys Ala Asn Ser Tyr Ile Ile Arg Ile Ser Lys Ser Phe Leu Asp Leu Gln Lys Asp Phe Asp Asn Ala Thr Leu Val Asn Thr Ser Ser Leu Lys Pro Lys Glu Ala Gly Ser Asp Glu Asn Phe Glu Phe Lys Pro Glu Pro Phe Arg Ile Glu Asn Gly Thr Asn Phe Tyr Ile Ala Val Gln Ala Ile Asn Glu Ala Asn Leu Thr Ser Glu Val Ser Asn 

ä ..

Ile Ala Gln Ala Ile Lys Phe Ile Pro Met Pro Glu Asp Ser Val Pro

Ala Leu Gly Thr Lys Ile Ser Ala Ile Asn Leu Ala Ile Phe Ala Leu 885 890 895

Ala Met Ile Leu Ser Ile Val 900

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